

CRF Errors Corrected by the STIC System Branch

Serial Number: 09/692,945

CRF Processing Date: APR 22 2003

Edited by: DC

Verified by: DC

RECEIVED

APR 22 2003

ENTERED

TECH CENTER 1600/2900

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_.
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☐ Other: \_\_\_\_\_

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95



APR 22 2003

OIEP

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## RAW SEQUENCE LISTING

DATE: 04/15/2003

PATENT APPLICATION: US/09/692,945

TIME: 13:13:12

Input Set : A:\PTO.DC.txt

Output Set: N:\CRF4\04152003\I692945.raw

```

4 <110> APPLICANT: Chiron Corporation
5     Kyoto University
6     Itoh, Nobuyuki
7     Kavanaugh, Michael W.
9 <120> TITLE OF INVENTION: HUMAN FGF-20 GENE AND GENE EXPRESSION
10    PRODUCTS
12 <130> FILE REFERENCE: 60219-6/16770.001
14 <140> CURRENT APPLICATION NUMBER: 09/692,945
15 <141> CURRENT FILING DATE: 2000-10-20
17 <160> NUMBER OF SEQ ID NOS: 17
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 648
23 <212> TYPE: DNA
24 <213> ORGANISM: Rattus norvegicus
26 <400> SEQUENCE: 1
27 ccttccatgg ctcccttgac cgaagtcggt gccttcttgg gcggcctgga gggcttgggc      60
28 cagcaggtgg ggtcgcactt cttgctgcct cctgcagggg agcgaccgcc gctgctaggg      120
29 gagcggcggg gcgcgttgga gcggggcgcc cgcgggcggg cggttccgt ggagctggcg      180
30 cacctgcacg gcctcctgcg ccgccggcag ctctactgcc gcaccggctt ccacctgcag      240
31 atcctgcccg acggcagtggt gcagggcacc cggcaggatc acagcctctt cggtatcctg      300
32 gaattcatca gtgtggcggt ggggctggtc agtatcagag gtgtggacag cggcctgtac      360
33 cttggcatga atggcaaagg agagctttat ggctcagaga aattgacttc tgaatgcac      420
34 ttcagggaac aatttgaaga gaactggtat aatacctatt catccaacat atacaaacac      480
35 ggagacacag gtcgcaggta tttttagtga ctttaaaaag acgggactcc aagggacggt      540
36 gccaggtcca aaagacacca aaagtttacc cattttttac ccagaccagt ggaccagag      600
37 agagtcccag agttatacaa agacctactg gtgtacactg gatgaacc      648
39 <210> SEQ ID NO: 2
40 <211> LENGTH: 212
41 <212> TYPE: PRT
42 <213> ORGANISM: Rattus norvegicus
44 <400> SEQUENCE: 2
45 Met Ala Pro Leu Thr Glu Val Gly Ala Phe Leu Gly Gly Leu Glu Gly
46 1          5          10          15
47 Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu Pro Pro Ala Gly Glu
48          20          25          30
49 Arg Pro Pro Leu Leu Gly Glu Arg Arg Gly Ala Leu Glu Arg Gly Ala
50          35          40          45
51 Arg Gly Gly Pro Gly Ser Val Glu Leu Ala His Leu His Gly Ile Leu
52          50          55          60
53 Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu
54 65          70          75          80
55 Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly

```

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56          85          90          95
57 Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly
58          100          105          110
59 Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Gly Lys Gly Glu Leu Tyr
60          115          120          125
61 Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu
62          130          135          140
63 Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp
64 145          150          155          160
65 Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg
66          165          170          175
67 Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro
68          180          185          190
69 Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asp Leu Leu
70          195          200          205
71 Val Tyr Thr Gly
72          210
74 <210> SEQ ID NO: 3
75 <211> LENGTH: 636
76 <212> TYPE: DNA
77 <213> ORGANISM: Homo sapiens
79 <400> SEQUENCE: 3
80 atggctccct tagccgaagt cgggggcttt ctgggcggcc tggagggtt gggccagcag      60
81 gtgggttcgc atttctgtt gctcctgcc ggggagcggc cgccgtgct gggcgagcgc      120
82 aggagcgcg cggagcggag cgcgcgcggc gggccggggg ctgcgcagct ggcgcacctg      180
83 cacggcatcc tgcgcgcgg gcagctctat tgccgcaccg gcttcacact gcagatcctg      240
84 cccgacggca gcgtgcagg caccgcgcag gaccacagcc tcttcggtat cttggaattc      300
85 atcagtgtgg cagtgggact ggtcagtatt agagggtgtg acagtgggtc ctatcttgga      360
86 atgaatgaca aaggagaact ctatggatca gagaaactta cttccgaatg catctttagg      420
87 gagcagtttg aagagaactg gtataacacc tattcatcta acatatataa acatggagac      480
88 actggccgca ggtattttgt ggcacttaac aaagacggaa ctccaagaga tggcgccagg      540
89 tccaagaggc atcagaaatt tacacatttc ttacctagac cagtggatcc agaaagagtt      600
90 ccagaattgt acaaggacct actgatgtac acttga      636
92 <210> SEQ ID NO: 4
93 <211> LENGTH: 211
94 <212> TYPE: PRT
95 <213> ORGANISM: Homo sapiens
97 <400> SEQUENCE: 4
98 Met Ala Pro Leu Ala Glu Val Gly Gly Phe Leu Gly Gly Leu Glu Gly
99 1          5          10          15
100 Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu Pro Pro Ala Gly Glu
101          20          25          30
102 Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala Ala Glu Arg Ser Ala
103          35          40          45
104 Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly Ile Leu
105          50          55          60
106 Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu
107 65          70          75          80
108 Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly

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109                85                90                95
110 Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly
111                100                105                110
112 Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr
113                115                120                125
114 Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu
115                130                135                140
116 Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp
117 145                150                155                160
118 Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg
119                165                170                175
120 Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro
121                180                185                190
122 Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asp Leu Leu
123                195                200                205
124 Met Tyr Thr
125                210
127 <210> SEQ ID NO: 5
128 <211> LENGTH: 14
129 <212> TYPE: PRT
130 <213> ORGANISM: Artificial Sequence
132 <220> FEATURE:
133 <223> OTHER INFORMATION: Oligopeptides for raising antibodies
135 <400> SEQUENCE: 5
136 Arg Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His
137 1                5                10
139 <210> SEQ ID NO: 6
140 <211> LENGTH: 15
141 <212> TYPE: PRT
142 <213> ORGANISM: Artificial Sequence
144 <220> FEATURE:
145 <223> OTHER INFORMATION: Oligopeptides for raising antibodies
147 <400> SEQUENCE: 6
148 Gln Leu Ala His Leu His Gly Ile Leu Arg Arg Arg Gln Leu Tyr
149 1                5                10                15
151 <210> SEQ ID NO: 7
152 <211> LENGTH: 10
153 <212> TYPE: PRT
154 <213> ORGANISM: Artificial Sequence
156 <220> FEATURE:
157 <223> OTHER INFORMATION: Residues which can be incorporated into FGF-20 to
158 allow myc monoclonal antibody-based affinity
159 purification.
161 <400> SEQUENCE: 7
162 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
163 1                5                10
165 <210> SEQ ID NO: 8
166 <211> LENGTH: 5
167 <212> TYPE: PRT

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Output Set: N:\CRF4\04152003\I692945.raw

168 <213> ORGANISM: Artificial Sequence  
170 <220> FEATURE:  
171 <223> OTHER INFORMATION: Preferred thrombin cleavage site.  
173 <400> SEQUENCE: 8  
174 Leu Val Pro Arg Gly  
175 1 5  
177 <210> SEQ ID NO: 9  
178 <211> LENGTH: 10  
179 <212> TYPE: PRT  
180 <213> ORGANISM: Artificial Sequence  
182 <220> FEATURE:  
183 <223> OTHER INFORMATION: Sequence which can be incorporated to allow for  
184 pufication of FGF-20 because of its ablility to  
185 bind to paramagnetic streptavidin beads.  
187 <400> SEQUENCE: 9  
188 Ser Ala Trp Arg His Pro Gln Phe Gly Gly  
189 1 5 10  
191 <210> SEQ ID NO: 10  
192 <211> LENGTH: 6  
193 <212> TYPE: PRT  
194 <213> ORGANISM: Artificial Sequence  
196 <220> FEATURE:  
197 <223> OTHER INFORMATION: Consensus amino acid sequences used to create  
198 sense and anti-sense PCR primers.  
200 <400> SEQUENCE: 10  
201 Phe Glu Glu Asn Trp Tyr  
202 1 5  
204 <210> SEQ ID NO: 11  
205 <211> LENGTH: 6  
206 <212> TYPE: PRT  
207 <213> ORGANISM: Artificial Sequence  
209 <220> FEATURE:  
210 <223> OTHER INFORMATION: Consensus amino acid sequences used to create  
211 sense and anti-sense PCR primers.  
213 <400> SEQUENCE: 11  
214 Thr His Phe Leu Pro Arg  
215 1 5  
217 <210> SEQ ID NO: 12  
218 <211> LENGTH: 6  
219 <212> TYPE: PRT  
220 <213> ORGANISM: Artificial Sequence  
222 <220> FEATURE:  
223 <223> OTHER INFORMATION: Consensus amino acid sequences used to create  
224 sense and anti-sense PCR primers.  
226 <400> SEQUENCE: 12  
227 Glu Asn Trp Tyr Asn Thr  
228 1 5  
230 <210> SEQ ID NO: 13  
231 <211> LENGTH: 6

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232 <212> TYPE: PRT
233 <213> ORGANISM: Artificial Sequence
235 <220> FEATURE:
236 <223> OTHER INFORMATION: Consensus amino acid sequences used to create
237     sense and anti-sense PCR primers.
239 <400> SEQUENCE: 13
240 His Gln Lys Phe Thr His
241 1           5
243 <210> SEQ ID NO: 14
244 <211> LENGTH: 13
245 <212> TYPE: PRT
246 <213> ORGANISM: Artificial Sequence
248 <220> FEATURE:
249 <223> OTHER INFORMATION: E-tag
251 <400> SEQUENCE: 14
252 Gly Ala Pro Val Pro Tyr Pro Asp Pro Leu Glu Pro Arg
253 1           5           10
255 <210> SEQ ID NO: 15
256 <211> LENGTH: 6
257 <212> TYPE: PRT
258 <213> ORGANISM: Artificial Sequence
260 <220> FEATURE:
261 <223> OTHER INFORMATION: His tag
263 <400> SEQUENCE: 15
264 His His His His His His
265 1           5
267 <210> SEQ ID NO: 16
268 <211> LENGTH: 208
269 <212> TYPE: PRT
270 <213> ORGANISM: Rattus norvegicus
272 <400> SEQUENCE: 16
273 Met Ala Pro Leu Gly Glu Val Gly Ser Tyr Phe Gly Val Gln Asp Ala
274 1           5           10           15
275 Val Pro Phe Gly Asn Val Pro Val Leu Pro Val Asp Ser Pro Val Leu
276     20           25           30
277 Leu Ser Asp His Leu Gly Gln Ser Glu Ala Gly Gly Leu Pro Arg Gly
278     35           40           45
279 Pro Ala Val Thr Asp Leu Asp His Leu Lys Gly Ile Leu Arg Arg Arg
280     50           55           60
281 Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Glu Ile Phe Pro Asn Gly
282 65           70           75           80
283 Thr Ile Gln Gly Thr Arg Lys Asp His Ser Arg Phe Gly Ile Leu Glu
284     85           90           95
285 Phe Ile Ser Ile Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser
286     100          105          110
287 Gly Leu Tyr Leu Gly Met Asn Glu Lys Gly Glu Leu Tyr Gly Ser Glu
288     115          120          125
289 Lys Leu Thr Gln Glu Cys Val Phe Arg Glu Gln Phe Glu Glu Asn Trp
290     130          135          140

```

**VERIFICATION SUMMARY**

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Output Set: N:\CRF4\04152003\I692945.raw